



SEQUENCE LISTING

<110> Odgren, Paul R.
Marks, Sandy C.
Choi, Yongwon

<120> TRANCE REGULATION OF CHONDROCYTE
DIFFERENTIATION

<130> 07917-120001

<140> 09/933,915

<141> 2001-08-20

<150> 60/226,197

<151> 2000-08-18

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2226

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (157)...(1107)

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agggaggaga	gctccgaagc	gagagggccg	agcgcc atg	cgc cgc gcc	agc aga	174
			Met Arg Arg	Ala Ser Arg		
			1	5		

gac tac acc aag tac ctg cgt ggc tgc gag gag atg ggc ggc ggc ccc	222
Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu Glu Met Gly Gly Gly Pro	
10 15 20	

gga gcc ccg cac gag ggc ccc ctg cac gcc ccg ccg ccg cct gcg ccg	270
Gly Ala Pro His Glu Gly Pro Leu His Ala Pro Pro Pro Pro Ala Pro	
25 30 35	

cac cag ccc ccc gcc gcc tcc cgc tcc atg ttc gtg gcc ctc ctg ggg	318
His Gln Pro Pro Ala Ala Ser Arg Ser Met Phe Val Ala Leu Leu Gly	
40 45 50	

ctg ggg ctg ggc cag gtt gtc tgc agc gtc gcc ctg ttc ttc tat ttc	366
Leu Gly Leu Gly Gln Val Val Cys Ser Val Ala Leu Phe Phe Tyr Phe	
55 60 65 70	

aga gcg cag atg gat cct aat aga ata tca gaa gat ggc act cac tgc	414
Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys	
75 80 85	



1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYF
71 RAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHI
141 RAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQ
211 DGFYYLYANICFRHHETSGDLATEYLQIMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF
281 FKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID (SEQ ID NO:2)

FIG. 2

att tat aga att ttg aga ctc cat gaa aat gca gat ttt caa gac aca Ile Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr 90 95 100	462
act ctg gag agt caa gat aca aaa tta ata cct gat tca tgt agg aga Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg 105 110 115	510
att aaa cag gcc ttt caa gga gct gtg caa aag gaa tta caa cat atc Ile Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile 120 125 130	558
gtt gga tca cag cac atc aga gca gag aaa gcg atg gtg gat ggc tca Val Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser 135 140 145 150	606
tgg tta gat ctg gcc aag agg agc aag ctt gaa gct cag cct ttt gct Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala 155 160 165	654
cat ctc act att aat gcc acc gac atc cca tct ggt tcc cat aaa gtg His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val 170 175 180	702
agt ctg tcc tct tgg tac cat gat cgg ggt tgg gcc aag atc tcc aac Ser Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn 185 190 195	750
atg act ttt agc aat gga aaa cta ata gtt aat cag gat ggc ttt tat Met Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr 200 205 210	798
tac ctg tat gcc aac att tgc ttt cga cat cat gaa act tca gga gac Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp 215 220 225 230	846
cta gct aca gag tat ctt caa cta atg gtg tac gtc act aaa acc agc Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser 235 240 245	894
atc aaa atc cca agt tct cat acc ctg atg aaa gga gga agc acc aag Ile Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys 250 255 260	942
tat tgg tca ggg aat tct gaa ttc cat ttt tat tcc ata aac gtt ggt Tyr Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly 265 270 275	990
gga ttt ttt aag tta cgg tct gga gag gaa atc agc atc gag gtc tcc Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser 280 285 290	1038
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ttt aaa gtt cga gat ata gat tgagccccag tttttggagt gttatgtatt 1137
 Phe Lys Val Arg Asp Ile Asp
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tcctggatgt ttggaaacat tttttaaaac aagccaagaa agatgtatat aggtgtgtga 1197
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 gccactgaaa tctgtcaaga gtagttatat aattgttgaa caggtgtttt tccacaagtg 2037
 ccgcaaatg tacctttttt tttttttcaa aatagaaaag ttattagtgg tttatcagca 2097
 aaaaagtcca attttaattt agtaaatgtt atcttatact gtacaataaa aacattgcct 2157
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 aaaaaaaaaa 2226

<210> 2
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 <213> Homo sapiens

<400> 2
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 1 5 10 15
 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20 25 30
 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35 40 45
 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 50 55 60
 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85 90 95
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His

210	215	220
His Glu Thr Ser Gly Asp	Leu Ala Thr Glu Tyr	Leu Gln Leu Met Val
225	230	235
Tyr Val Thr Lys Thr Ser	Ile Lys Ile Pro Ser	Ser His Thr Leu Met
245	250	255
Lys Gly Gly Ser Thr Lys	Tyr Trp Ser Gly Asn	Ser Glu Phe His Phe
260	265	270
Tyr Ser Ile Asn Val Gly	Gly Phe Phe Lys Leu	Arg Ser Gly Glu Glu
275	280	285
Ile Ser Ile Glu Val Ser	Asn Pro Ser Leu Leu	Asp Pro Asp Gln Asp
290	295	300
Ala Thr Tyr Phe Gly Ala	Phe Lys Val Arg Asp	Ile Asp
305	310	315

<210> 3
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 <213> Homo Sapiens

<400> 3
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20 25 30
Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr
35 40 45
Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His
50 55 60
Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys
65 70 75 80
Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys
85 90 95
Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln
100 105 110
Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His
115 120 125
Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu
130 135 140
Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser
145 150 155 160
Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro
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Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
180 185 190

<210> 4
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 <212> PRT
 <213> Homo sapiens

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20 25 30
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
35 40 45

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
 50 55 60
 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
 65 70 75 80
 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
 85 90 95
 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
 100 105 110
 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
 115 120 125
 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
 130 135 140
 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
 145 150 155 160
 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
 165 170 175
 Val Arg Asp Ile Asp
 180

<210> 5
 <211> 178
 <212> PRT
 <213> Homo sapiens

<400> 5
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 20 25 30
 Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp
 35 40 45
 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn
 50 55 60
 Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
 65 70 75 80
 Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr
 85 90 95
 Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser
 100 105 110
 Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn
 115 120 125
 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
 130 135 140
 Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu
 145 150 155 160
 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp
 165 170 175
 Ile Asp

<210> 6
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 <212> PRT
 <213> Homo sapiens

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			20					25					30			
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
		35					40					45				
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val	
	50					55					60					
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
65					70				75						80	
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val	
				85					90					95		
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met	
			100					105					110			
Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
		115					120					125				
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu	
	130					135					140					
Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
145					150					155					160	
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp				
				165					170							

<210> 7
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 <213> Homo sapiens

<400> 7																
Ser	Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	
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Asp	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	
		20						25					30			
Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	
		35					40					45				
Leu	Ile	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	
	50					55					60					
Phe	Arg	His	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	
65					70				75						80	
Leu	Met	Val	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	
				85					90					95		
Thr	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	
			100					105				110				
Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	
		115					120					125				
Gly	Glu	Glu	Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	
	130					135					140					
Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp	
145					150					155					160	

<210> 8
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 <212> PRT
 <213> Homo sapiens

<400> 8																
Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	
1				5					10					15		

Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp
 20 25 30
 Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu
 35 40 45
 Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe
 50 55 60
 Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu
 65 70 75 80
 Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr
 85 90 95
 Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe
 100 105 110
 His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly
 115 120 125
 Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp
 130 135 140
 Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 145 150 155

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<220>
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 <222> (95)...(826)

<221> misc_feature
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 Met Asp Pro Asn Arg Ile Ser
 1 5

 gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa aat 163
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 10 15 20

 gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta ata 211
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 25 30 35

 cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg caa 259
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 40 45 50 55

 aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag aaa 307
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 60 65 70

 gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag ctt 355
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 75 80 85

gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc cca Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro 90 95 100	403
tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg ggt Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly 105 110 115	451
tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata gtt Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val 120 125 130 135	499
aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga cat Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 140 145 150	547
cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg gtg His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val 155 160 165	595
tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg atg Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met 170 175 180	643
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ttattagtgg tttatcagca aaaaagtcca attttaattt agtaaagtgtt atcttatact 1856
gtacaataaaa aacattgcct ttgaatgtta attttttggt acaaaaataa atttatatga 1916
aaacctgaaa aaaaaaaciaa aaaaaaaaaa 1945

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<210> 10
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<212> PRT
<213> Homo sapiens

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 20          25          30
Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln
 35          40          45
Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser
 50          55          60
Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp
 65          70          75          80
Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr
 85          90          95
Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser
100         105         110
Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe
115         120         125
Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr
130         135         140
Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr
145         150         155         160
Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile
165         170         175
Pro Ser Ser His Thr Leu Met Lys Gly Ser Thr Lys Tyr Trp Ser
180         185         190
Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe
195         200         205
Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser
210         215         220
Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val
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Arg Asp Ile Asp

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<210> 11
<211> 3136
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (39)...(1886)

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Met Ala Pro Arg Ala Arg
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cgg cgc cgc ccg ctg ttc gcg ctg ctg ctg ctc tgc gcg ctg ctc gcc Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu Ala 10 15 20	104
cgg ctg cag gtg gct ttg cag atc gct cct cca tgt acc agt gag aag Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys 25 30 35	152
cat tat gag cat ctg gga cgg tgc tgt aac aaa tgt gaa cca gga aag His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys 40 45 50	200
tac atg tct tct aaa tgc act act acc tct gac agt gta tgt ctg ccc Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro 55 60 65 70	248
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ttg ctg cat aaa gtt tgt gat aca ggc aag gcc ctg gtg gcc gtg gtc Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val 90 95 100	344
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gaa cat cat ggg aca gag aaa tcc gat gcg gtt tgc agt tct tct ctg Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu 185 190 195	632
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 20           25           30
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
 35           40           45
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50           55           60
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65           70           75           80
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85           90           95
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100          105          110
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115          120          125
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130          135          140
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145          150          155          160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165          170          175
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180          185          190
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195          200          205
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His

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210	215	220
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr		
225	230	235
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys		240
	245	250
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr		255
	260	265
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile		270
	275	280
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala		285
	290	295
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp		300
305	310	315

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